Thomas J Hudson

List of Publications by Year
in descending order

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114 papers	29,784 citations	15504 65 h-index	20961 115 g-index
118 all docs	118 docs citations	118 times ranked	41273 citing authors

#	Article	IF	Citations
1	Molecular and Pathology Features of Colorectal Tumors and Patient Outcomes Are Associated with Fusobacterium nucleatum and Its Subspecies animalis. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 210-220.	2.5	19
2	Genetic Regulation of DNA Methylation Yields Novel Discoveries in GWAS of Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1068-1076.	2.5	1
3	Association between germline variants and somatic mutations in colorectal cancer. Scientific Reports, 2022, 12, .	3.3	1
4	Identifying colorectal cancer caused by biallelic MUTYH pathogenic variants using tumor mutational signatures. Nature Communications, 2022, 13, .	12.8	15
5	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	12.1	44
6	Cumulative Burden of Colorectal Cancerâ€“Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	1.3	110
7	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	12.8	55
8	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
9	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
10	Activation of hedgehog signaling associates with early disease progression in chronic lymphocytic leukemia. Blood, 2019, 133, 2651-2663.	1.4	15
11	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
12	Simulating thermal effects of <scp>MR</scp>â€guided focused ultrasound in cortical bone and its surrounding tissue. Medical Physics, 2018, 45, 506-519.	3.0	10
13	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
14	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538.	17.5	273
15	Genome-Wide DNA Methylation Analysis Reveals Epigenetic Dysregulation of MicroRNA-34A in TP53-Associated Cancer Susceptibility. Journal of Clinical Oncology, 2016, 34, 3697-3704.	1.6	33
16	Common variants in the obesity-associated genes FTO and MC4R are not associated with risk of colorectal cancer. Cancer Epidemiology, 2016, 44, 1-4.	1.9	12
17	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	1.3	97
18	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. PLoS Genetics, 2016, 12, e1006296.	3.5	38

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19	Transcriptome-wide characterization of the endogenous miR-34A-p53 tumor suppressor network. Oncotarget, 2016, 7, 49611-49622.	1.8	9
20	GLI2 inhibition abrogates human leukemia stem cell dormancy. Journal of Translational Medicine, 2015, 13, 98.	4.4	80
21	Spatial genomic heterogeneity within localized, multifocal prostate cancer. Nature Genetics, 2015, 47, 736-745.	21.4	395
22	Meta-analysis identifies seven susceptibility loci involved in the atopic march. Nature Communications, 2015, 6, 8804.	12.8	148
23	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
24	The effect of 5-fluorouracil/leucovorin chemotherapy on CpG methylation, or the confounding role of leukocyte heterogeneity: An illustration. Genomics, 2015, 106, 340-347.	2.9	6
25	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
26	Long-range epigenetic regulation is conferred by genetic variation located at thousands of independent loci. Nature Communications, 2015, 6, 6326.	12.8	115
27	Association of Aspirin and NSAID Use With Risk of Colorectal Cancer According to Genetic Variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133.	7.4	171
28	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. Human Genetics, 2015, 134, 1249-1262.	3.8	28
29	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. Carcinogenesis, 2015, 36, 999-1007.	2.8	28
30	No Evidence of Geneâ€“Calcium Interactions from Genome-Wide Analysis of Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2971-2976.	2.5	9
31	Identification of pre-leukaemic haematopoietic stem cells in acute leukaemia. Nature, 2014, 506, 328-333.	27.8	1,241
32	A Pan-BCL2 Inhibitor Renders Bone-Marrow-Resident Human Leukemia Stem Cells Sensitive to Tyrosine Kinase Inhibition. Cell Stem Cell, 2013, 12, 316-328.	11.1	167
33	Discovery of cross-reactive probes and polymorphic CpGs in the Illumina Infinium HumanMethylation450 microarray. Epigenetics, 2013, 8, 203-209.	2.7	1,276
34	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292
35	Analysis of early C2C12 myogenesis identifies stably and differentially expressed transcriptional regulators whose knock-down inhibits myoblast differentiation. Physiological Genomics, 2012, 44, 183-197.	2.3	33
36	Meta-analysis of new genome-wide association studies of colorectal cancer risk. Human Genetics, 2012, 131, 217-234.	3.8	183

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37	MLH1 Region Polymorphisms Show a Significant Association with CpG Island Shore Methylation in a Large Cohort of Healthy Individuals. PLoS ONE, 2012, 7, e51531.	2.5	17
38	Genetic Variants and Susceptibility to Neurological Complications Following West Nile Virus Infection. Journal of Infectious Diseases, 2011, 204, 1031-1037.	4.0	37
39	Cancer genome variation in children, adolescents, and young adults. Cancer, 2011, 117, 2262-2267.	4.1	4
40	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
41	A cis-Acting Regulatory Variant in the IL2RA Locus. Journal of Immunology, 2009, 183, 5158-5162.	0.8	20
42	Identification of susceptibility genes for complex diseases using pooling-based genome-wide association scans. Human Genetics, 2009, 125, 305-318.	3.8	74
43	Analyses of associations with asthma in four asthma population samples from Canada and Australia. Human Genetics, 2009, 125, 445-459.	3.8	95
44	CAG Expansion in the Huntington Disease Gene Is Associated with a Specific and Targetable Predisposing Haplogroup. American Journal of Human Genetics, 2009, 84, 351-366.	6.2	204
45	Asthma and genes encoding components of the vitamin D pathway. Respiratory Research, 2009, 10, 98.	3.6	121
46	Personalized medicine: A transformative approach is needed. Cmaj, 2009, 180, 911-913.	2.0	8
47	A genome-wide approach to identifying novel-imprinted genes. Human Genetics, 2008, 122, 625-634.	3.8	70
48	Replication of an association between 17q21 SNPs and asthma in a French-Canadian familial collection. Human Genetics, 2008, 123, 93-95.	3.8	61
49	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. Nature Genetics, 2008, 40, 631-637.	21.4	542
50	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
51	Identification of a chromosome 8p locus for early-onset coronary heart disease in a French Canadian population. European Journal of Human Genetics, 2008, 16, 105-114.	2.8	17
52	Genetic variation in immune signaling genes differentially expressed in asthmatic lung tissues. Journal of Allergy and Clinical Immunology, 2008, 122, 529-536.e17.	2.9	14
53	Allele-specific expression in the germline of patients with familial pancreatic cancer: An unbiased approach to cancer gene discovery. Cancer Biology and Therapy, 2008, 7, 135-144.	3.4	42
54	Disruption of AP1S1, Causing a Novel Neurocutaneous Syndrome, Perturbs Development of the Skin and Spinal Cord. PLoS Genetics, 2008, 4, e1000296.	3.5	131

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55	Differential Allelic Expression in the Human Genome: A Robust Approach To Identify Genetic and Epigenetic Cis-Acting Mechanisms Regulating Gene Expression. PLoS Genetics, 2008, 4, e1000006.	3.5	199
56	Sex-stratified Linkage Analysis Identifies a Female-specific Locus for IgE to Cockroach in Costa Ricans. American Journal of Respiratory and Critical Care Medicine, 2008, 177, 830-836.	5.6	71
57	Correction of Population Stratification in Large Multi-Ethnic Association Studies. PLoS ONE, 2008, 3, e1382.	2.5	60
58	Genes to Diseases (G2D) Computational Method to Identify Asthma Candidate Genes. PLoS ONE, 2008, 3, e2907.	2.5	35
59	Toward Further Mapping of the Association Between the IL2RA Locus and Type 1 Diabetes. Diabetes, 2007, 56, 1174-1176.	0.6	82
60	1Î±,25-Dihydroxy-vitamin D3 stimulation of bronchial smooth muscle cells induces autocrine, contractility, and remodeling processes. Physiological Genomics, 2007, 29, 161-168.	2.3	123
61	Association of Urokinase-type Plasminogen Activator with Asthma and Atopy. American Journal of Respiratory and Critical Care Medicine, 2007, 175, 1109-1116.	5.6	47
62	Patterns of variation in DNA segments upstream of transcription start sites. Human Mutation, 2007, 28, 441-450.	2.5	4
63	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2007, 39, 989-994.	21.4	676
64	A genome-wide association study identifies novel risk loci for type 2 diabetes. Nature, 2007, 445, 881-885.	27.8	2,651
65	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
66	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
67	A genetic linkage map of the vervet monkey (Chlorocebus aethiops sabaeus). Mammalian Genome, 2007, 18, 347-360.	2.2	55
68	Detection and characterization of DNA variants in the promoter regions of hundreds of human disease candidate genes. Genomics, 2006, 87, 704-710.	2.9	26
69	Mapping cis-acting regulatory variation in recombinant congenic strains. Physiological Genomics, 2006, 25, 294-302.	2.3	20
70	Influence of human genome polymorphism on gene expression. Human Molecular Genetics, 2006, 15, R9-R16.	2.9	115
71	An Evaluation of the Performance of Tag SNPs Derived from HapMap in a Caucasian Population. PLoS Genetics, 2006, 2, e27.	3.5	105
72	PRKCA and Multiple Sclerosis: Association in Two Independent Populations. PLoS Genetics, 2006, 2, e42.	3.5	45

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73	Resources for Genetic Variation Studies. Annual Review of Genomics and Human Genetics, 2006, 7, 443-457.	6.2	14
74	A predominant role for the HLA class II region in the association of the MHC region with multiple sclerosis. Nature Genetics, 2005, 37, 1108-1112.	21.4	295
75	An atypical form of erythrokeratodermia variabilis maps to chromosome 7q22. Human Genetics, 2005, 116, 167-171.	3.8	33
76	Anatomy of a founder effect: myotonic dystrophy in Northeastern Quebec. Human Genetics, 2005, 117, 177-187.	3.8	54
77	Survey of allelic expression using EST mining. Genome Research, 2005, 15, 1584-1591.	5.5	115
78	Mapping common regulatory variants to human haplotypes. Human Molecular Genetics, 2005, 14, 3963-3971.	2.9	84
79	Functional promoter SNPs in cell cycle checkpoint genes. Human Molecular Genetics, 2005, 14, 2641-2648.	2.9	28
80	A Predominantly Clonal Multi-Institutional Outbreak ofClostridium difficileâ€“Associated Diarrhea with High Morbidity and Mortality. New England Journal of Medicine, 2005, 353, 2442-2449.	27.0	1,829
81	Characterization of a Common Susceptibility Locus for Asthma-Related Traits. Science, 2004, 304, 300-304.	12.6	442
82	Functional classes of bronchial mucosa genes that are differentially expressed in asthma. BMC Genomics, 2004, 5, 21.	2.8	106
83	Cis-Acting Regulatory Variation in the Human Genome. Science, 2004, 306, 647-650.	12.6	241
84	Association of Vitamin D Receptor Genetic Variants with Susceptibility to Asthma and Atopy. American Journal of Respiratory and Critical Care Medicine, 2004, 170, 967-973.	5.6	217
85	A survey of genetic and epigenetic variation affecting human gene expression. Physiological Genomics, 2004, 16, 184-193.	2.3	228
86	Wanted: regulatory SNPs. Nature Genetics, 2003, 33, 439-440.	21.4	98
87	Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 605-610.	7.1	526
88	5' Flanking Variants of Resistin Are Associated With Obesity. Diabetes, 2002, 51, 1629-1634.	0.6	158
89	Polymorphisms in Toll-Like Receptor 4 Are Not Associated with Asthma or Atopy-related Phenotypes. American Journal of Respiratory and Critical Care Medicine, 2002, 166, 1449-1456.	5.6	154
90	Characterization of Variability in Large-Scale Gene Expression Data: Implications for Study Design. Genomics, 2002, 79, 104-113.	2.9	178

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91	A Missense Mutation (R565W) in Cirhin (FLJ14728) in North American Indian Childhood Cirrhosis. American Journal of Human Genetics, 2002, 71, 1443-1449.	6.2	106
92	A Second-Generation Association Study of the 5q31 Cytokine Gene Cluster and the Interleukin-4 Receptor in Asthma. Genomics, 2001, 77, 35-42.	2.9	46
93	A Sequence Variation in the Mitochondrial Glycerol-3-Phosphate Dehydrogenase Gene Is Associated with Increased Plasma Glycerol and Free Fatty Acid Concentrations among French Canadians. Molecular Genetics and Metabolism, 2001, 72, 209-217.	1.1	9
94	A Novel Syndrome Affecting Multiple Mitochondrial Functions, Located by Microcell-Mediated Transfer to Chromosome 2p14-2p13. American Journal of Human Genetics, 2001, 68, 386-396.	6.2	70
95	A Genomewide Linkage-Disequilibrium Scan Localizes the Saguenayâ€“Lac-Saint-Jean Cytochrome Oxidase Deficiency to 2p16. American Journal of Human Genetics, 2001, 68, 397-409.	6.2	39
96	A Progressive Autosomal Recessive Cataract Locus Maps to Chromosome 9q13-q22. American Journal of Human Genetics, 2001, 68, 772-777.	6.2	46
97	Manganese superoxide dismutase induction by iron is impaired in Friedreich ataxia cells. FEBS Letters, 2001, 509, 101-105.	2.8	71
98	A susceptibility locus for asthma-related traits on chromosome 7 revealed by genome-wide scan in a founder population. Nature Genetics, 2001, 28, 87-91.	21.4	168
99	A radiation hybrid map of mouse genes. Nature Genetics, 2001, 29, 201-205.	21.4	93
100	Title is missing!. Nature Genetics, 2001, 28, 87-91.	21.4	75
101	ARSACS, a spastic ataxia common in northeastern QuÃ©bec, is caused by mutations in a new gene encoding an 11.5-kb ORF. Nature Genetics, 2000, 24, 120-125.	21.4	395
102	Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse. Nature Genetics, 2000, 24, 381-386.	21.4	395
103	The common PPARÎ³ Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. Nature Genetics, 2000, 26, 76-80.	21.4	1,672
104	Complete nucleotide sequence and genomic structure of the human NRAMP1 gene region on Chromosome region 2q35. Mammalian Genome, 2000, 11, 755-762.	2.2	28
105	Localization of a Recessive Gene for North American Indian Childhood Cirrhosis to Chromosome Region 16q22â€”and Identification of a Shared Haplotype. American Journal of Human Genetics, 2000, 67, 222-228.	6.2	40
106	An Optimized Set of Human Telomere Clones for Studying Telomere Integrity and Architecture. American Journal of Human Genetics, 2000, 67, 320-332.	6.2	284
107	Radiation hybrid map of the mouse genome. Nature Genetics, 1999, 22, 384-387.	21.4	110
108	A YAC-based physical map of the mouse genome. Nature Genetics, 1999, 22, 388-393.	21.4	84

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109	Location Score and Haplotype Analyses of the Locus for Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay, in Chromosome Region 13q11. American Journal of Human Genetics, 1999, 64, 768-775.	6.2	80
110	Autosomal Recessive Spastic Ataxia of Charlevoixâ€“Saguenay (ARSACS): High-Resolution Physical and Transcript Map of the Candidate Region in Chromosome Region 13q11. Genomics, 1999, 62, 156-164.	2.9	25
111	Autosomal recessive spastic ataxia of Charlevoixâ€“Saguenay. Neuromuscular Disorders, 1998, 8, 474-479.	0.6	122
112	Genomewide Scan of Multiple Sclerosis in Finnish Multiplex Families. American Journal of Human Genetics, 1997, 61, 1379-1387.	6.2	284
113	Characterization of Short Tandem Repeats from Thirty-One Humanâ€‰Telomeres. Genome Research, 1997, 7, 917-923.	5.5	37
114	A PCR-Based Linkage Map of Human Chromosome 1. Genomics, 1993, 15, 251-258.	2.9	42